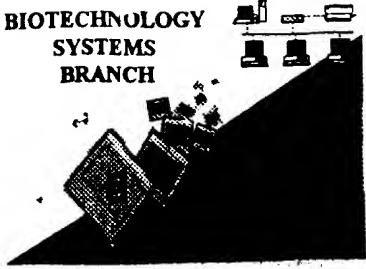


strzelecka

#11

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable format:

Application Serial Number: 09/530,746

Source: 1656

Date Processed by STIC: 4/30/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) NOTIFYING THE APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/536,746</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of "Artificial" (NEW RULES)	Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing) Instead, please use "File Manager" or any other means to copy file to floppy disk.	

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817.QQ.txt
Output Set: N:\CRF3\04302001\I530746.raw

JP 1-4

Does Not Comply

Corrected Diskette Needed

3 <110> APPLICANT: Kessler, Christoph
4 Haberhausen, Gerd
5 Bartl, Knut
6 Orum, Henrik
8 <120> TITLE OF INVENTION: SPECIFIC AND SENSITIVE NUCLEIC ACID DETECTION METHOD
11 <130> FILE REFERENCE: 4817/QQ
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/530,746
C--> 14 <141> CURRENT FILING DATE: 2000-11-16
16 <150> NUMBER OF SEQ ID NOS: 94
18 <170> SOFTWARE: PatentIn Version 3.0

ERRORED SEQUENCES

248 <210> SEQ ID NO: 21
249 <211> LENGTH: 21
250 <212> TYPE: DNA
C--> 251 <213> ORGANISM: Artificial item 11
253 <220> FEATURE:
254 <223> OTHER INFORMATION: amplification primer
256 <400> SEQUENCE: 21
E--> 257 cgtactgcct iatagggtt do not show "i" in the sequence itself. Use "n" and explain in
260 <210> SEQ ID NO: 22
261 <211> LENGTH: 23
262 <212> TYPE: DNA item 11
C--> 263 <213> ORGANISM: Artificial item 11
265 <220> FEATURE:
266 <223> OTHER INFORMATION: amplification primer
268 <400> SEQUENCE: 22
E--> 269 gmatgtgmta mggtmtmid gdc invalid - use n and explain 23
272 <210> SEQ ID NO: 23
273 <211> LENGTH: 20
274 <212> TYPE: DNA
C--> 275 <213> ORGANISM: Artificial item 11
277 <220> FEATURE:
278 <223> OTHER INFORMATION: amplification primer
280 <400> SEQUENCE: 23
E--> 281 cgtactgcct iatagggtt invalid 20
284 <210> SEQ ID NO: 24
285 <211> LENGTH: 21
286 <212> TYPE: DNA
C--> 287 <213> ORGANISM: Artificial item 11
289 <220> FEATURE:
290 <223> OTHER INFORMATION: amplification primer
292 <400> SEQUENCE: 24
E--> 293 cgtamtgmmt iatagggtt invalid 21
296 <210> SEQ ID NO: 25

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817.QQ.txt
Output Set: N:\CRF3\04302001\1530746.raw

297 <211> LENGTH: 23
298 <212> TYPE: DNA
C--> 299 <213> ORGANISM: Artificial *new 11*
301 <220> FEATURE:
302 <223> OTHER INFORMATION: amplification primer
304 <400> SEQUENCE: 25
E--> 305 gmatgppa mggtmtddid gdm *invalid-use "n" and explain* 23
308 <210> SEQ ID NO: 16
309 <211> LENGTH: 26
310 <212> TYPE: DNA
C--> 311 <213> ORGANISM: Artificial *new 11*
313 <220> FEATURE:
314 <223> OTHER INFORMATION: amplification primer
316 <400> SEQUENCE: 26
E--> 317 cgtamtgmmt iatagggtim *invalid* 20
332 <210> SEQ ID NO: 28
333 <211> LENGTH: 21
334 <212> TYPE: DNA
C--> 335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: amplification primer
340 <400> SEQUENCE: 28
E--> 341 cgtamtgmmt iatagggtic t *invalid* 21
344 <210> SEQ ID NO: 29
345 <211> LENGTH: 26
346 <212> TYPE: DNA
C--> 347 <213> ORGANISM: Artificial
349 <220> FEATURE:
350 <223> OTHER INFORMATION: amplification primer
352 <400> SEQUENCE: 29
E--> 353 gmatgtgmta mggtmtddid gdm ttc 26
356 <210> SEQ ID NO: 30
357 <211> LENGTH: 20
358 <212> TYPE: DNA
C--> 359 <213> ORGANISM: Artificial
361 <220> FEATURE:
362 <223> OTHER INFORMATION: amplification primer
364 <400> SEQUENCE: 30
E--> 365 cgtamtgmmt iatagggtic *invalid* 20
368 <210> SEQ ID NO: 31
369 <211> LENGTH: 26
370 <212> TYPE: DNA
C--> 371 <213> ORGANISM: Artificial
373 <220> FEATURE:
374 <223> OTHER INFORMATION: amplification primer
376 <400> SEQUENCE: 31
E--> 377 gmatgtgmta mggtmtddid gdm tcc 26
380 <210> SEQ ID NO: 32
381 <211> LENGTH: 26

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 14/11/2001
TIME: 17:59:38

Input Set: A:\4817_0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

482 <211> TYPE: DNA 26
C--> 383 <213> ORGANISM: Artificial
485 <211> FEATURE
386 <213> OTHER INFORMATION: amplification primer
388 <400> SEQUENCE 32 *involved*
E--> 389 gmatgpkppa mggtmtdmid gdmpm 26
416 <210> SEQ ID NO: 35
417 <211> LENGTH: 18
418 <212> TYPE: DNA
C--> 419 <213> ORGANISM: Artificial
421 <211> FEATURE
422 <213> OTHER INFORMATION: amplification primer
424 <400> SEQUENCE 35 *involved* 18
E--> 425 cgtamtgmmnt *ataggggt* *involved* 18
428 <210> SEQ ID NO: 36
429 <211> LENGTH: 17
430 <212> TYPE: DNA
C--> 431 <213> ORGANISM: Artificial
433 <211> FEATURE
434 <213> OTHER INFORMATION: amplification primer
436 <400> SEQUENCE 36 *involved* 27
E--> 437 gmatgtgmma mgltmtamia gamttmc 27
440 <210> SEQ ID NO: 37
441 <211> LENGTH: 27
442 <212> TYPE: DNA
C--> 443 <213> ORGANISM: Artificial
445 <211> FEATURE
446 <213> OTHER INFORMATION: amplification primer
448 <400> SEQUENCE 37 *involved* 27
E--> 449 gmatgtgmma mggtmtamia gamptmc 27
452 <210> SEQ ID NO: 38
453 <211> LENGTH: 27
454 <212> TYPE: DNA
C--> 455 <213> ORGANISM: Artificial
457 <211> FEATURE
458 <213> OTHER INFORMATION: amplification primer
460 <400> SEQUENCE 38 *involved* 27
E--> 461 gmatgtgmma mggtmtamia gamptmm 27
464 <210> SEQ ID NO: 39
465 <211> LENGTH: 18
466 <212> TYPE: DNA
C--> 467 <213> ORGANISM: Artificial
469 <211> FEATURE
470 <213> OTHER INFORMATION: amplification primer
472 <400> SEQUENCE 39 *involved* 18
E--> 473 cgtdmtgmmnt *idtdgggt* *involved* 18
476 <210> SEQ ID NO: 40
477 <211> LENGTH: 27
478 <212> TYPE: DNA

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:38

Input Set : A:\4817 0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

```
C--> 479 <213> ORGANISM: Artificial
481 <213> FEATURE:
482 <213> OTHER INFORMATION: amplification primer
484 <400> SEQUENCE: 40
E--> 485 gmatgpkppa mgitmtamia gamptmc → invalid 27
512 <210> SEQ ID NO: 41
513 <211> LENGTH: 27
514 <212> TYPE: DNA
C--> 491 <213> ORGANISM: Artificial
493 <220> FEATURE:
494 <223> OTHER INFORMATION: amplification primer
496 <400> SEQUENCE: 41
E--> 497 gmatgpkppa mggtmtamia gamptmm → invalid 27
512 <210> SEQ ID NO: 43
513 <211> LENGTH: 27
514 <212> TYPE: DNA
C--> 515 <213> ORGANISM: Artificial
517 <220> FEATURE:
518 <223> OTHER INFORMATION: amplification primer
520 <400> SEQUENCE: 43
E--> 521 gmatgtgma mggtnmtimga gaamtmc → invalid 27
524 <210> SEQ ID NO: 44
525 <211> LENGTH: 27
526 <212> TYPE: DNA
C--> 527 <213> ORGANISM: Artificial ← These two error types exist
529 <220> FEATURE: throughout Sequence Listing
530 <223> OTHER INFORMATION: amplification primer
532 <400> SEQUENCE: 44 → invalid 27
E--> 533 gmatgtgma mggtnmtimga gakmtmc
114.9 <210> SEQ ID NO: 93
1110 <211> LENGTH: 61
1111 <212> TYPE: DNA
1112 <213> ORGANISM: HCV
1114 <400> SEQUENCE: 93
E--> 1115 gttactgcct gatagggtgc ttgcgagtc cccggggagg t ctcgttagacc
E--> 1116 gtgcaccatg a
1119 <210> SEQ ID NO: 94
1120 <211> LENGTH: 61
1121 <212> TYPE: DNA
1122 <213> ORGANISM: HGBV-B
1124 <400> SEQUENCE: 94
E--> 1125 cgtactgcct gatagggtcc ttgcgagggg atctggggagt ctcgttagacc
E--> 1126 gtagcacatg c
```

The types of errors shown exist throughout the Sequence Listing. Please check
all sequences for similar errors.

← 50 ← insert cumulative
61 base total at
right margin of
each line

(61) 50
61 ←

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/530,746

DATE: 04/30/2001
TIME: 17:59:34

Input Set : A:\4817_0Q.txt
Output Set: N:\CRF3\04302001\I530746.raw

L:13 M:171 C: Current Application Number differs. Replaced Current Application Number
L:14 M:171 C: Current Filing Date differs. Replaced Current Filing Date
L:23 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:1
L:35 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:2
L:47 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:3
L:59 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:4
L:71 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:5
L:119 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:10
L:131 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:11
L:143 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:12
L:155 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:13
L:167 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:14
L:179 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:15
L:191 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:16
L:203 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:17
L:215 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:18
L:227 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:19
L:239 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:20
L:251 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:21
L:357 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:263 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:22
L:269 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:275 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:23
L:281 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:287 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:24
L:293 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:299 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:25
L:305 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:311 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:26
L:317 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:323 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:27
L:345 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:28
L:341 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:347 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:29
L:353 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:359 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:30
L:365 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:371 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:31
L:377 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:383 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:32
L:389 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:395 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:33
L:407 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:34
L:419 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:35
L:425 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:431 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:36
L:437 M:221 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:443 M:221 C: Keyword misspelled or invalid format. <213> ORGANISM for SEQ ID#:37

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/530,746

DATE: 14/30/2001

TIME: 17:59:39

Input Set : A:\4817_0Q.txt

Output Set: N:\CRF3\04302001\I530746.raw

L:449 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:455 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:38
L:461 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:467 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:39
L:473 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:479 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:40
L:485 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
L:491 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:41
L:497 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:503 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:42
L:515 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:43
L:521 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:527 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:44
L:533 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:549 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:45
L:545 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:551 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:46
L:563 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:47
L:569 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:575 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:48
L:581 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:587 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:49
L:593 M:220 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:4
L:599 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:50
L:611 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:51
L:623 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:52
L:635 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:53
L:647 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:54
L:1115 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:93
M:254 Repeated in SeqNo=93
L:3125 M:254 E: No. of Bases conflict, LENGTH:Input:61 Counted:50 SEQ:94
M:254 Repeated in SeqNo=94